

## SEQUENCE LISTING

&lt;110&gt; Aventis Pasteur Limited

&lt;120&gt; Chlamydia antigens and corresponding DNA fragments and uses thereof

&lt;130&gt; 77813-13

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; US 60/132,270

&lt;151&gt; 1999-05-03

&lt;150&gt; US 60/141,276

&lt;151&gt; 1999-06-30

&lt;160&gt; 14

&lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 2156

&lt;212&gt; DNA

&lt;213&gt; Chlamydia pneumoniae

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)...(2053)

&lt;400&gt; 1

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				Met Val Asn Pro Ile	
				1 5	

ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt	163
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu	
10 15 20	

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct	211
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala	
25 30 35	

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat	259
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp	
40 45 50	

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg	307
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met	
55 60 65	

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct	355
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser	
70 75 80 85	

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act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg	403
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr	
90 95 100	
cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct	451
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala	
105 110 115	
tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct	499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala	
120 125 130	
ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct	547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala	
135 140 145	
act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc	595
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala	
150 155 160 165	
gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct	643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala	
170 175 180	
tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc	691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe	
185 190 195	
gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa	739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys	
200 205 210	
gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg	787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly	
215 220 225	
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca	835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr	
230 235 240 245	
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt	883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe	
250 255 260	
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac	931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn	
265 270 275	
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag	979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys	
280 285 290	
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt	1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu	
295 300 305	

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caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat	1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn	
310 315 320 325	
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt	1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val	
330 335 340	
gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc	1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser	
345 350 355	
atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct	1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser	
360 365 370	
ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct	1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser	
375 380 385	
caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc	1315
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala	
390 395 400 405	
gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct	1363
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala	
410 415 420	
tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat	1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn	
425 430 435	
gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt cct	1459
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro	
440 445 450	
ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag	1507
Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys	
455 460 465	
acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt	1555
Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly	
470 475 480 485	
tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga aat	1603
Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn	
490 495 500	
gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc aca	1651
Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr	
505 510 515	
cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca	1699
Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr	
520 525 530	

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gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt gga 1747  
 Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly  
 535 540 545

gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc 1795  
 Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile  
 550 555 560 565

cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca 1843  
 Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr  
 570 575 580

tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt 1891  
 Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu  
 585 590 595

tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt 1939  
 Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe  
 600 605 610

gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa 1987  
 Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu  
 615 620 625

acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta 2035  
 Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu  
 630 635 640 645

tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 2083  
 Tyr Ser Gly Tyr Leu Gln  
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ttattatgtg ctttggaag gcctttgttg aggccttacc aacacactag aacgatcttc 2143

aataaataaaa aga 2156

<210> 2  
 <211> 651  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 2  
 Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr  
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 Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn  
 20 25 30  
 Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys  
 35 40 45  
 Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala  
 50 55 60

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Val	Asn	Ala	Leu	Met	Ser	Leu	Ala	Asp	Lys	Leu	Gly	Ile	Ala	Ser	Ser	65	70	75	80
Asn	Ser	Ser	Ser	Ser	Thr	Ser	Arg	Ser	Ala	Asp	Val	Asp	Ser	Thr	Thr	85	90	95	
Ala	Thr	Ala	Pro	Thr	Pro	Pro	Pro	Pro	Thr	Phe	Asp	Asp	Tyr	Lys	Thr	100	105	110	
Gln	Ala	Gln	Thr	Ala	Tyr	Asp	Thr	Ile	Phe	Thr	Ser	Thr	Ser	Leu	Ala	115	120	125	
Asp	Ile	Gln	Ala	Ala	Leu	Val	Ser	Leu	Gln	Asp	Ala	Val	Thr	Asn	Ile	130	135	140	
Lys	Asp	Thr	Ala	Ala	Thr	Asp	Glu	Glu	Thr	Ala	Ile	Ala	Ala	Glu	Trp	145	150	155	160
Glu	Thr	Lys	Asn	Ala	Asp	Ala	Val	Lys	Val	Gly	Ala	Gln	Ile	Thr	Glu	165	170	175	
Leu	Ala	Lys	Tyr	Ala	Ser	Asp	Asn	Gln	Ala	Ile	Leu	Asp	Ser	Leu	Gly	180	185	190	
Lys	Leu	Thr	Ser	Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	195	200	205	
Ala	Asn	Asn	Asn	Lys	Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	210	215	220	
Pro	Val	Val	Pro	Gly	Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	225	230	235	240
Gln	Thr	Asp	Ala	Thr	Ala	Thr	Gln	Ile	Glu	Lys	Asp	Gly	Asn	Ala	Ile	245	250	255	
Arg	Asp	Ala	Tyr	Phe	Ala	Gly	Gln	Asn	Ala	Ser	Gly	Ala	Val	Glu	Asn	260	265	270	
Ala	Lys	Ser	Asn	Asn	Ser	Ile	Ser	Asn	Ile	Asp	Ser	Ala	Lys	Ala	Ala	275	280	285	
Ile	Ala	Thr	Ala	Lys	Thr	Gln	Ile	Ala	Glu	Ala	Gln	Lys	Lys	Phe	Pro	290	295	300	
Asp	Ser	Pro	Ile	Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	305	310	315	320
Lys	Asp	Leu	Lys	Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	325	330	335	
Pro	Gly	Thr	Thr	Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	340	345	350	

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Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala  
355 360 365

Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr  
370 375 380

Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala  
385 390 395 400

Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala  
405 410 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln  
420 425 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val  
435 440 445

Ser Ala Gly Val Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val  
450 455 460

Lys Gln Leu Tyr Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr  
465 470 475 480

Gln Ile Ser Ala Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr  
485 490 495

Gly Arg Ala Arg Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser  
500 505 510

Thr Pro Ala Leu Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg  
515 520 525

Gly Pro Glu Lys Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn  
530 535 540

Ser Arg Thr Leu Gly Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser  
545 550 555 560

Val Met Gln Ile Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile  
565 570 575

Arg Gln Lys Leu Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr  
580 585 590

Pro Tyr Val Gln Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys  
595 600 605

Leu Glu Ser Leu Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys  
610 615 620

Ala Leu Ser Phe Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val  
625 630 635 640

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Asn Ile Gly Ser Leu Tyr Ser Gly Tyr Leu Gln  
645 650

<210> 3  
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<212> DNA  
<213> Chlamydia pneumoniae  
<220> 1842  
<221> CDS  
<222> (101..(2053)

<400> 3  
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tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct 96  
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro  
20 25 30  
acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca 144  
Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr  
35 40 45  
gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct 192  
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala  
50 55 60  
gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg 240  
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala  
65 70 75 80  
gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat 288  
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn  
85 90 95  
gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat 336  
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr  
100 105 110  
gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc 384  
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser  
115 120 125  
ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac 432  
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn  
130 135 140  
aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca 480  
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro  
145 150 155 160  
ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct 528  
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala  
165 170 175

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aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat	576
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr	
180 190 195	
ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat	624
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn	
200 205 210	
aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct	672
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala	
215 220 225	
aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att	720
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile	
230 235 240 245	
ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa	768
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys	
250 255 260	
aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca	816
Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr	
265 270 275	
gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt	864
Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val	
280 285 290	
tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg	912
Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met	
295 300 305	
tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat	960
Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp	
310 315 320 325	
tct caa gct gcc caa cag gag ctg gca gca caa gct aga gca gcg aaa	1008
Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys	
330 335 340	
gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa	1056
Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys	
345 350 355	
gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctg	1104
Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu	
360 365 370	
aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt	1152
Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val	
375 380 385	
Cct ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac	1200
Pro Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr	
390 395 400 405	

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aag acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca 1248  
 Lys Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala  
 410 415 420

ggt tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga 1296  
 Gly Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg  
 425 430 435

aat gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc 1344  
 Asn Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu  
 440 445 450

aca cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa 1392  
 Thr Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys  
 455 460 465

aca gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt 1440  
 Thr Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu  
 470 475 480 485

gga gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc 1488  
 Gly Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile  
 490 495 500

act cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt 1536  
 Ile Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu  
 505 510 515

aca tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa 1584  
 Thr Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln  
 520 525 530

ctt tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg 1632  
 Leu Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu  
 535 540 545

ttt gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt 1670  
 Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe  
 550 555 560 565

gaa acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct 1718  
 Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser  
 570 575 580

cta tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 1769  
 Leu Tyr Ser Gly Tyr Leu Gln  
 585

ttattatgtg ctttggttaag gcctttgttg aggccttacc aacacactag aacgatcttc 1829

aataaataaaa aga 1842

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<210> 4

<211> 583

<212> PRT

<213> Chlamydia pneumoniae

<400> 4

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20 25 30

Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr  
35 40 45

Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala  
50 55 60

Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala  
65 70 75 80

Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn  
85 90 95

Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr  
100 105 110

Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser  
115 120 125

Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn  
130 135 140

Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro  
145 150 155 160

Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala  
165 170 175

Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr  
180 185 190

Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn  
195 200 205

Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala  
210 215 220

Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile  
225 230 235 240

Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys  
245 250 255

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Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	Pro	Gly	Thr	Thr		
			260					265					270				
Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	Ser	Ile	Arg	Val		
		275					280					285					
Ser	Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	Ser	Ile	Leu	Met		
	290					295					300						
Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	Glu	Asn	Pro	Asp		
305					310					315					320		
Ser	Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	Arg	Ala	Ala	Lys		
				325					330					335			
Ala	Ala	Gly	Asp	Asp	Ser	Ala	Ala	Ala	Ala	Leu	Ala	Asp	Ala	Gln	Lys		
			340					345					350				
Ala	Leu	Glu	Ala	Ala	Leu	Gly	Lys	Ala	Gly	Gln	Gln	Gln	Gly	Ile	Leu		
		355					360						365				
Asn	Ala	Leu	Gly	Gln	Ile	Ala	Ser	Ala	Ala	Val	Val	Ser	Ala	Gly	Val		
	370					375					380						
Pro	Pro	Ala	Ala	Ala	Ser	Ser	Ile	Gly	Ser	Ser	Val	Lys	Gln	Leu	Tyr		
385					390					395					400		
Lys	Thr	Ser	Lys	Ser	Thr	Gly	Ser	Asp	Tyr	Lys	Thr	Gln	Ile	Ser	Ala		
				405					410					415			
Gly	Tyr	Asp	Ala	Tyr	Lys	Ser	Ile	Asn	Asp	Ala	Tyr	Gly	Arg	Ala	Arg		
			420					425					430				
Asn	Asp	Ala	Thr	Arg	Asp	Val	Ile	Asn	Asn	Val	Ser	Thr	Pro	Ala	Leu		
		435					440					445					
Thr	Arg	Ser	Val	Pro	Arg	Ala	Arg	Thr	Glu	Ala	Arg	Gly	Pro	Glu	Lys		
	450					455					460						
Thr	Asp	Gln	Ala	Leu	Ala	Arg	Val	Ile	Ser	Gly	Asn	Ser	Arg	Thr	Leu		
465					470					475					480		
Gly	Asp	Val	Tyr	Ser	Gln	Val	Ser	Ala	Leu	Gln	Ser	Val	Met	Gln	Ile		
				485					490					495			
Ile	Gln	Ser	Asn	Pro	Gln	Ala	Asn	Asn	Glu	Glu	Ile	Arg	Gln	Lys	Leu		
			500					505					510				
Thr	Ser	Ala	Val	Thr	Lys	Pro	Pro	Gln	Phe	Gly	Tyr	Pro	Tyr	Val	Gln		
		515					520					525					
Leu	Ser	Asn	Asp	Ser	Thr	Gln	Lys	Phe	Ile	Ala	Lys	Leu	Glu	Ser	Leu		
		530				535					540						

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Phe Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe  
545 550 555 560

Glu Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser  
565 570 575

Leu Tyr Ser Gly Tyr Leu Gln  
580

<210> 5  
<211> 1456  
<212> DNA  
<213> Chlamydia pneumoniae

<220>  
<221> CDS  
<222> (101)..(1456)

<400> 5  
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ataataaaac taaaagattt ttattatttt ttgagttttt atg gtt aat cct att 115  
Met Val Asn Pro Ile  
1 5  
ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt 163  
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu  
10 15 20  
tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct 211  
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala  
25 30 35  
caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat 259  
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp  
40 45 50  
tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg 307  
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met  
55 60 65  
agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct 355  
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser  
70 75 80 85  
act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg 403  
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr  
90 95 100  
cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct 451  
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala  
105 110 115

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tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct	499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala	
120 125 130	
ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct	547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala	
135 140 145	
act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc	595
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala	
150 155 160 165	
gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct	643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala	
170 175 180	
tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc	691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe	
185 190 195	
gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa	739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys	
200 205 210	
gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg	787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly	
215 220 225	
aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca	835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr	
230 235 240 245	
gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt	883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe	
250 255 260	
gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac	931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn	
265 270 275	
agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag	979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys	
280 285 290	
aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt	1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu	
295 300 305	
caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat	1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn	
310 315 320 325	
atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt	1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val	
330 335 340	

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gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc 1171  
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser  
345 350 355

atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct 1219  
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser  
360 365 370

ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct 1267  
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser  
375 380 385

caa gct gcc caa cag gag ctg gca gca caa gct aga gca gcg aaa gcc 1315  
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala  
390 395 400 405

gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct 1363  
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala  
410 415 420

tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctg aat 1411  
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn  
425 430 435

gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta 1456  
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val  
440 445 450

<210> 6

<211> 452

<212> PRT

<213> Chlamydia pneumoniae

<400> 6

Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr  
1 5 10 15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn  
20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys  
35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala  
50 55 60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser  
65 70 75 80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr  
85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr  
100 105 110

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Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala  
115 120 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile  
130 135 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp  
145 150 155 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu  
165 170 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly  
180 185 190

Lys Leu Thr Ser Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val  
195 200 205

Ala Asn Asn Asn Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn  
210 215 220

Pro Val Val Pro Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp  
225 230 235 240

Gln Thr Asp Ala Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile  
245 250 255

Arg Asp Ala Tyr Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn  
260 265 270

Ala Lys Ser Asn Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala  
275 280 285

Ile Ala Thr Ala Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro  
290 295 300

Asp Ser Pro Ile Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu  
305 310 315 320

Lys Asp Leu Lys Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn  
325 330 335

Pro Gly Thr Thr Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly  
340 345 350

Ser Ile Arg Val Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala  
355 360 365

Ser Ile Leu Met Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr  
370 375 380

Glu Asn Pro Asp Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala  
385 390 395 400

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Arg Ala Ala Lys Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala  
 405 410 415

Asp Ala Gln Lys Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln  
 420 425 430

Gln Gly Ile Leu Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val  
 435 440 445

Ser Ala Gly Val  
 450

<210> 7  
 <211> 2238  
 <212> DNA  
 <213> Chlamydia pneumoniae

<220>  
 <221> CDS  
 <222> (766) .. (2235)

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 ttttttgtga aatgtagtgt tgcgactgg aacacattcg ttccttcaga aacctccact 120  
 acagaaaaag ctgctacaaa cgctatgaaa tacaataact gtgtttggca gtggctcgtc 180  
 ggaaagcata gtcagggtcc ttggatcaat ggacagaaaa agcctctata tctttatgga 240  
 gctttcttaa tgaacccttt agcaaaggct acgaagacta cgttaaatgg aaaagaaaac 300  
 ctagcttggt ttattggagg aactttaggg ggactcagaa aagctggaga ctggctcgcc 360  
 acagtacgtt atgagtatgt cgaagccttg tcggttccag aaatagatgt ttcagggatt 420  
 ggccgtggta atttattaaa gttttgggtc gcccaagcaa ttgctgctaa ctatgatcct 480  
 aaagaggcta atgggttttac aaattataaa ggattttccg ctctatatat gtatggcacc 540  
 acagattctc tatcattcag agcttatggg gcttactcca aaccagcaaa cgataaaactc 600  
 ggcagtgatt ttactttccg aaagtttgat ctaggtataa tttcagcggt ttaagtcaaa 660  
 ttttaataaa atctttaaaa acaggctcgc attaattatt agtgagagct ttttttttat 720  
 tttttataat aaaactaaaa gatttttatt attttttgag ttttt atg gtt aat cct 777  
 Met Val Asn Pro

1

att ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat 825  
 Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp  
 5 10 15 20

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ctt tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu	873
25 30 35	
gct caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr	921
40 45 50	
gat tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu	969
55 60 65	
atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser	1017
70 75 80	
tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro	1065
85 90 95 100	
acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr	1113
105 110 115	
gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala	1161
120 125 130	
gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala	1209
135 140 145	
gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn	1257
150 155 160	
gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr	1305
165 170 175 180	
gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser	1353
185 190 195	
ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn	1401
200 205 210	
aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro	1449
215 220 225	
ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala	1497
230 235 240	

10014630-121401

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aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat	1545
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr	
245 250 255 260	
ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat	1593
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn	
265 270 275	
aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct	1641
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala	
280 285 290	
aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att	1689
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile	
295 300 305	
ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa	1737
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys	
310 315 320	
aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca	1785
Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr	
325 330 335 340	
ggt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt	1833
Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val	
345 350 355	
tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg	1881
Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met	
360 365 370	
tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat	1929
Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp	
375 380 385	
tct caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa	1977
Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys	
390 395 400	
gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa	2025
Ala Ala Gly Asp Asp Ser Ala Ala Ala Leu Ala Asp Ala Gln Lys	
405 410 415 420	
gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc	2073
Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu	
425 430 435	
aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta	2121
Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val	
440 445 450	

10014570-101401

19/22

ctc ccg ctg cag caa gtt cta tgg atc cga gct cgg tac caa gct tac 2169  
 Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg Tyr Gln Ala Tyr  
 455 460 465

gta gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac 2217  
 Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp  
 470 475 480

cat cat cat cat cat cat tga 2238  
 His His His His His His  
 485 490

<210> 8  
 <211> 490  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 8  
 Met Val Asn Pro Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr  
 1 5 10 15

Pro Pro Ala Asp Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn  
 20 25 30

Lys Ser Ala Glu Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys  
 35 40 45

Glu Ser Lys Thr Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala  
 50 55 60

Val Asn Ala Leu Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser  
 65 70 75 80

Asn Ser Ser Ser Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr  
 85 90 95

Ala Thr Ala Pro Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr  
 100 105 110

Gln Ala Gln Thr Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala  
 115 120 125

Asp Ile Gln Ala Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile  
 130 135 140

Lys Asp Thr Ala Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp  
 145 150 155 160

Glu Thr Lys Asn Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu  
 165 170 175

Leu Ala Lys Tyr Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly  
 180 185 190

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Lys	Leu	Thr	Ser	Phe	Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	195	200	205
Ala	Asn	Asn	Asn	Lys	Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	210	215	220
Pro	Val	Val	Pro	Gly	Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	225	230	235
Gln	Thr	Asp	Ala	Thr	Ala	Thr	Gln	Ile	Glu	Lys	Asp	Gly	Asn	Ala	Ile	245	250	255
Arg	Asp	Ala	Tyr	Phe	Ala	Gly	Gln	Asn	Ala	Ser	Gly	Ala	Val	Glu	Asn	260	265	270
Ala	Lys	Ser	Asn	Asn	Ser	Ile	Ser	Asn	Ile	Asp	Ser	Ala	Lys	Ala	Ala	275	280	285
Ile	Ala	Thr	Ala	Lys	Thr	Gln	Ile	Ala	Glu	Ala	Gln	Lys	Lys	Phe	Pro	290	295	300
Asp	Ser	Pro	Ile	Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	305	310	315
Lys	Asp	Leu	Lys	Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	325	330	335
Pro	Gly	Thr	Thr	Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	340	345	350
Ser	Ile	Arg	Val	Ser	Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	355	360	365
Ser	Ile	Leu	Met	Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	370	375	380
Glu	Asn	Pro	Asp	Ser	Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	385	390	395
Arg	Ala	Ala	Lys	Ala	Ala	Gly	Asp	Asp	Ser	Ala	Ala	Ala	Ala	Leu	Ala	405	410	415
Asp	Ala	Gln	Lys	Ala	Leu	Glu	Ala	Ala	Leu	Gly	Lys	Ala	Gly	Gln	Gln	420	425	430
Gln	Gly	Ile	Leu	Asn	Ala	Leu	Gly	Gln	Ile	Ala	Ser	Ala	Ala	Val	Val	435	440	445
Ser	Ala	Gly	Val	Leu	Pro	Leu	Gln	Gln	Val	Leu	Trp	Ile	Arg	Ala	Arg	450	455	460
Tyr	Gln	Ala	Tyr	Val	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	465	470	475
																		480

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Ser Ala Val Asp His His His His His  
485 490

<210> 9  
<211> 43  
<212> DNA  
<213> primer

<400> 9

ataagaatgc ggccgccacc atggttaate ctattgtcc agg

43

<210> 10  
<211> 35  
<212> DNA  
<213> primer

<400> 10

gcgcggatc ccttggagat aaccagaata tagag

35

<210> 11  
<211> 43  
<212> DNA  
<213> primer

<400> 11

ataagaatgc ggccgccacc atgagtctgg cagataagct ggg

43

<210> 12  
<211> 32  
<212> DNA  
<213> primer

<400> 12

gcgcggatc ccttggagat aaccagaata ta

32

<210> 13  
<211> 38  
<212> DNA  
<213> primer

<400> 13

gctctagacc gccatgacaa aaaaacatta tgcttggg

38

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<210> 14  
<211> 28  
<212> DNA  
<213> primer

<400> 14

cgggatccat agaacttgct gcagcggg

28

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